

SEQUENCE LISTING

<110> Horvath, Christopher J.
Rao, Patricia E.

<120> Method of Inhibiting Stenosis and
Restenosis

<130> 1855.1069-003

<140> US 09/809,739

<141> 2001-03-15

<150> US 09/528,267

<151> 2000-03-17

<160> 23

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 125

<212> PRT

<213> Unknown

<220>

<221> SITE

<222> (1)...(125)

<223> YFC51.1 light chain variable region with signal
sequence

<221> SIGNAL

<222> (1)...(20)

<223> Rat

<400> 1

Met	Arg	Val	Gln	Val	Gln	Phe	Leu	Gly	Leu	Leu	Leu	Leu	Trp	Thr	Ser
1				5					10					15	
Gly	Ala	Gln	Cys	Asp	Val	Gln	Met	Thr	Gln	Ser	Pro	Ser	Tyr	Leu	Ala
			20					25					30		
Ala	Ser	Pro	Gly	Glu	Ser	Val	Ser	Ile	Ser	Cys	Lys	Ala	Ser	Lys	Ser
		35					40				45				
Ile	Ser	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Glu	Ala	Asn
	50					55				60					
Lys	Leu	Leu	Val	Tyr	Tyr	Gly	Ser	Thr	Leu	Arg	Ser	Gly	Ile	Pro	Ser
65				70					75					80	
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Arg
			85					90					95		
Asn	Leu	Glu	Pro	Ala	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Tyr
			100					105					110		
Glu	Arg	Pro	Leu	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	Glu			
		115					120					125			

<210> 2

<211> 11

<212> PRT

<213> Unknown

<220>

<221> SITE

<222> (1)...(11)

<223> CDR1 of YFC51.1 light chain

<223> Rat

<400> 2

Lys Ala Ser Lys Ser Ile Ser Asn Tyr Leu Ala
1 5 10

<210> 3

<211> 7

<212> PRT

<213> Unknown

<220>

<221> SITE

<222> (1)...(7)

<223> CDR2 of YFC51.1 light chain

<223> Rat

<400> 3

Tyr Gly Ser Thr Leu Arg Ser
1 5

<210> 4

<211> 9

<212> PRT

<213> Unknown

<220>

<221> SITE

<222> (1)...(9)

<223> CDR3 of YFC51.1 light chain

<223> Rat

<400> 4

Gln Gln Tyr Tyr Glu Arg Pro Leu Thr
1 5

<210> 5

<211> 139

<212> PRT

<213> Unknown

<220>

<221> SITE

<222> (1)...(139)

<223> YFC51.1 heavy chain variable region

<221> SIGNAL

<222> (1) ... (19)

<223> Rat

<400> 5

Met	Lys	Cys	Ser	Trp	Ile	Asn	Leu	Phe	Leu	Met	Ala	Leu	Ala	Ser	Gly
1				5					10					15	
Val	Tyr	Ala	Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Arg	Arg
			20					25					30		
Pro	Gly	Ser	Ser	Val	Lys	Leu	Ser	Cys	Lys	Thr	Ser	Gly	Tyr	Ser	Ile
		35					40					45			
Lys	Asp	Tyr	Leu	Leu	His	Trp	Val	Lys	His	Arg	Pro	Glu	Tyr	Gly	Leu
	50					55					60				
Glu	Trp	Ile	Gly	Trp	Ile	Asp	Pro	Glu	Asp	Gly	Glu	Thr	Lys	Tyr	Gly
65					70					75					80
Gln	Lys	Phe	Gln	Ser	Arg	Ala	Thr	Leu	Thr	Ala	Asp	Thr	Ser	Ser	Asn
				85						90				95	
Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Asp	Asp	Thr	Ala	Thr
			100					105					110		
Tyr	Phe	Cys	Thr	Arg	Gly	Glu	Tyr	Arg	Tyr	Asn	Ser	Trp	Phe	Asp	Tyr
		115					120					125			
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser					
	130					135									

<210> 6

<211> 5

<212> PRT

<213> Unknown

 $\langle 220 \rangle$

<221> SITE

$\langle 222 \rangle$ (1) ... (5)

<223> CDR1 of YFC51.1 heavy chain

<223> Rat

<400> 6

Asp Tyr Leu Leu His
1 5

<210> 7

<211> 17

<212> PRT

<213> Unknown

 $\langle 220 \rangle$

<221> SITE

<222> (1) ... (17)

<223> CDR2 of YFC51.1 heavy chain

<223> Rat

<400> 7

Trp Ile Asp Pro Glu Asp Gly Glu Thr Lys Tyr Gly Gln Lys Phe Gln
1 5 10 15
Ser

<210> 8
 <211> 11
 <212> PRT
 <213> Unknown

<220>
 <221> SITE
 <222> (1)...(11)
 <223> CDR3 of YFC51.1 heavy chain

<223> Rat

<400> 8
 Gly Glu Tyr Arg Tyr Asn Ser Trp Phe Asp Tyr
 1 5 10

<210> 9
 <211> 139
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized heavy chain variable region with signal
 sequence

<400> 9
 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15
 Val His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
 20 25 30
 Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Thr Phe
 35 40 45
 Thr Asp Tyr Leu Leu His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu
 50 55 60
 Glu Trp Ile Gly Trp Ile Asp Pro Glu Asp Gly Glu Thr Lys Tyr Gly
 65 70 75 80
 Gln Lys Phe Gln Ser Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn
 85 90 95
 Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
 100 105 110
 Tyr Tyr Cys Ala Arg Gly Glu Tyr Arg Tyr Asn Ser Trp Phe Asp Tyr
 115 120 125
 Trp Gly Gln Gly Ser Leu Val Thr Val Ser Ser
 130 135

<210> 10
 <211> 127
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized light chain variable region with signal
 sequence

<221> SIGNAL
 <222> (1)...(19)

```

<400> 10
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1           5           10           15
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
           20           25           30
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Lys Ser Ile
           35           40           45
Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
           50           55           60
Leu Leu Ile Tyr Tyr Gly Ser Thr Leu Arg Ser Gly Val Pro Ser Arg
65           70           75           80
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
           85           90           95
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Glu
           100          105          110
Arg Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
           115          120          125

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<210> 11
<211> 112
<212> PRT
<213> Unknown

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<220>
<221> SITE
<222> (1)...(112)
<223> Murine mAb 1D9 light chain variable region

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<221> SITE
<222> (24)...(39)
<223> CDR1

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<221> SITE
<222> (55)...(61)
<223> CDR2

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<221> SITE
<222> (94)...(102)
<223> CDR3

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<223> Mouse

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```

<400> 11
Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Val Thr Val Gly
 1           5           10           15
His Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
           20           25           30
Asp Gly Lys Thr Phe Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser
           35           40           45
Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
           50           55           60
Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65           70           75           80
Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly
           85           90           95
Thr His Phe Pro Tyr Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys
           100          105          110

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<210> 12
<211> 117
<212> PRT
<213> Unknown

<220>
<221> SITE
<222> (1)...(117)
<223> Murine mAb 1D9 heavy chain variable region

<221> SITE
<222> (31)...(35)
<223> CDR1

<221> SITE
<222> (50)...(68)
<223> CDR2

<221> SITE
<222> (101)...(106)
<223> CDR3

<223> Mouse

<400> 12
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Lys Gly
1 5 10 15
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Asn Ala Tyr
20 25 30
Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Arg Ile Arg Thr Lys Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60
Ser Val Lys Asp Arg Tyr Thr Ile Ser Arg Asp Asp Ser Glu Ser Met
65 70 75 80
Leu Phe Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Met Tyr
85 90 95
Tyr Cys Val Thr Phe Tyr Gly Asn Gly Val Trp Gly Thr Gly Thr Thr
100 105 110
Val Thr Val Ser Ser
115

<210> 13
<211> 111
<212> PRT
<213> Homo sapiens

<400> 13
Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30
Asp Gly Asn Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45
Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Arg Asp Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

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Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly
85 90 95
Thr His Trp Pro Phe Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile
100 105 110

<210> 14
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized sequence

<400> 14
Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15
Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30
Asp Gly Lys Thr Phe Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45
Pro Arg Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95
Thr His Phe Pro Tyr Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105 110

<210> 15
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized sequence

<400> 15
Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15
Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30
Asp Gly Lys Thr Phe Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser
35 40 45
Pro Arg Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95
Thr His Phe Pro Tyr Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105 110

<210> 16
<211> 112
<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized sequence

<400> 16

Asp	Val	Val	Met	Thr	Gln	Ser	Pro	Leu	Ser	Leu	Pro	Val	Thr	Leu	Gly
1				5					10					15	
Gln	Pro	Ala	Ser	Ile	Ser	Cys	Lys	Ser	Ser	Gln	Ser	Leu	Leu	Asp	Ser
		20					25						30		
Asp	Gly	Lys	Thr	Phe	Leu	Asn	Trp	Leu	Leu	Gln	Arg	Pro	Gly	Gln	Ser
	35					40					45				
Pro	Arg	Arg	Leu	Ile	Tyr	Leu	Val	Ser	Lys	Leu	Asp	Ser	Gly	Val	Pro
	50					55					60				
Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile
65				70					75					80	
Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys	Trp	Gln	Gly
			85					90						95	
Thr	His	Phe	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Arg	Leu	Glu	Ile	Lys
			100					105						110	

<210> 17

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized sequence

<400> 17

Asp	Val	Val	Met	Thr	Gln	Ser	Pro	Leu	Ser	Leu	Pro	Val	Thr	Leu	Gly
1				5					10					15	
His	Pro	Ala	Ser	Ile	Ser	Cys	Lys	Ser	Ser	Gln	Ser	Leu	Leu	Asp	Ser
		20					25						30		
Asp	Gly	Lys	Thr	Phe	Leu	Asn	Trp	Leu	Leu	Gln	Arg	Pro	Gly	Gln	Ser
	35					40					45				
Pro	Arg	Arg	Leu	Ile	Tyr	Leu	Val	Ser	Lys	Leu	Asp	Ser	Gly	Val	Pro
	50					55					60				
Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile
65				70					75					80	
Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys	Trp	Gln	Gly
			85					90						95	
Thr	His	Phe	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Arg	Leu	Glu	Ile	Lys
			100					105						110	

<210> 18

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized sequence

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<400> 18

```
Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
 1          5          10          15
His Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
          20          25          30
Asp Gly Lys Thr Phe Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser
          35          40          45
Pro Arg Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
          50          55          60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65          70          75          80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly
          85          90          95
Thr His Phe Pro Tyr Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
          100          105          110
```

<210> 19

<211> 119

<212> PRT

<213> Homo sapiens

<400> 19

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1          5          10          15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Ala
          20          25          30
Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35          40          45
Gly Arg Ile Lys Ser Lys Thr Asp Gly Gly Thr Thr Asp Tyr Ala Ala
          50          55          60
Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65          70          75          80
Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
          85          90          95
Tyr Cys Thr Thr Asp Ser Leu Pro Pro His Arg Val Trp Gly Gln Gly
          100          105          110
Thr Leu Val Thr Val Ser Ser
          115
```

<210> 20

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized sequence

<400> 20

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1          5          10          15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
          20          25          30
Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35          40          45
Gly Arg Ile Arg Thr Lys Asn Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
          50          55          60
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Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80
Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95
Tyr Cys Thr Thr Phe Tyr Gly Asn Gly Val Trp Gly Gln Gly Thr Leu
100 105 110
Val Thr Val Ser Ser
115

<210> 21
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized sequence

<400> 21
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Asn Ala Tyr
20 25 30
Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Gly Arg Ile Arg Thr Lys Asn Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60
Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80
Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95
Tyr Cys Thr Thr Phe Tyr Gly Asn Gly Val Trp Gly Gln Gly Thr Leu
100 105 110
Val Thr Val Ser Ser
115

<210> 22
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized sequence

<400> 22
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Asn Ala Tyr
20 25 30
Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Arg Ile Arg Thr Lys Asn Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60
Ser Val Lys Asp Arg Tyr Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80
Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95

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Tyr Cys Thr Thr Phe Tyr Gly Asn Gly Val Trp Gly Gln Gly Thr Leu
100 105 110
Val Thr Val Ser Ser
115

<210> 23
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized sequence

<400> 23
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Asn Ala Tyr
20 25 30
Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Arg Ile Arg Thr Lys Asn Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60
Ser Val Lys Asp Arg Tyr Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80
Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95
Tyr Cys Val Thr Phe Tyr Gly Asn Gly Val Trp Gly Gln Gly Thr Leu
100 105 110
Val Thr Val Ser Ser
115